C. Remarks

The claims are 74-78, with claim 74 being independent. Reconsideration of the present claims is expressly requested.

Claims 74-76 and 78 stand rejected under 35 U.S.C. § 102(e) as being allegedly anticipated by U.S. Patent No. 6,476,215 B1 (Okamoto). Claims 74 and 75 stand rejected under 35 U.S.C. § 102(b) as being allegedly anticipated by U.S. Patent No. 5,545,531 (Rava). Claims 77 and 78 stand rejected under 35 U.S.C. § 103(a) as being allegedly obvious from Rava in view of U.S. Patent No. 5,807,522 (Brown). Claim 76 stands rejected under 35 U.S.C. § 103(a) as being allegedly obvious from Rava in view of U.S. Patent No. 5,700,637 (Southern). Claims 74, 75, 77, and 78 stand rejected under 35 U.S.C. § 103(a) as being allegedly obvious from Brown in view of Rava. Claim 76 stands rejected under 35 U.S.C. § 103(a) as being allegedly obvious from Brown in view of Rava and Southern. Claim 77 stands rejected under 35 U.S.C. § 103(a) as being allegedly obvious from Okamoto in view of Brown. The grounds of rejection are respectfully traversed.

Prior to addressing the merits of rejection, Applicants would like to briefly discuss some of the features of the presently claimed invention. That invention is related to a method of detecting a complex formed between an oligonucleotide having a known base sequence and an object that is to be identified via hybridization with the probe. In this method, a predetermined amount of a first liquid test sample and a predetermined amount of a second liquid test sample are spotted in each of a plurality of square sections so that the spot of the first liquid test sample and the spot of the second liquid test sample are

sufficiently spaced from each other within each of the square sections. One type of oligonucleotide is immobilized at a uniform density on the surface of each square section.

Okamoto, in Example 9, discloses that (i) one of three types of DNA probes (SEQ ID Nos. 9-11) was immobilized on the surface of each well, (ii) 100 pl/well of a solution containing a corresponding complementary ssDNA was supplied to each well, and (iii) plural solutions were supplied separately to the wells (col. 26, lines 43-51). Thus, it is clear that because only one sample is placed in each well, a well does not represent a square section as presently claimed in which spots of different samples are sufficiently spaced from each other to conduct a complex-forming reaction between the oligonucleotide and the object component in each spot.

Applicants respectfully submit that Okamoto does not disclose or even suggest such square sections. Even if assumed, *arguendo*, that each well can be considered a spot, Okamoto does not disclose arranging the wells into square sections, so that one type of oligonucleotide is present at a uniform surface density in each such square section, and spotting samples as presently claimed. Thus, Applicants respectfully submit that Okamoto cannot affect the patentability of the presently claimed invention.

Rava is directed to a device, which can be used to concurrently process multiple biological chip assays. Rava discloses a biological chip plate having, for example, 96 wells arranged in 8 rows and 12 columns. Each of the wells has a probe array, which may be different or the same among the plurality of wells.

In principle, one sample is introduced into a single well. While multiple samples may be introduced into a single well in some cases (col. 9, lines 4-8), the samples

will mix, and the mixture will react with the probe array. Since each well has a probe array, which typically comprises different probes at different positions rather than a uniform layer of probe molecules, it is pointless to place plural samples in a single well so that plural spots are spaced from each other. In fact, Rava specifically states that when multiple samples introduced into a single well produce a positive result for a particular characteristic, identification of the sample requires that the assay be rerun with only a single sample per each well (col. 9, lines 5-8).

Brown cannot cure the deficiencies of Okamoto and Rava, and vice versa. Brown, like the other references, fails to disclose or suggest application of two test sample to separate, individual spots in separate square sections, as claimed.

Southern fails to cure the deficiencies of the other references for essentially the same reasons. Southern is directed to an apparatus and method for analyzing a polynucleic sequence. Like Okamoto, Rava, and Brown, it fails to disclose or suggest spotting each of the two test samples in each section in separate, individual spots that are sufficiently spaced from each other within each section.

In sum, it is clear that neither of the cited references, whether considered separately or in any combination, discloses or suggests all of the presently claimed elements.

Wherefore, withdrawal of the outstanding rejections and expedient passage of the application to issue are respectfully requested.

Applicants' undersigned attorney may be reached in our New York office by telephone at (212) 218-2100. All correspondence should continue to be directed to our address given below.

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